LISTING OF CLAIMS

This Listing of Claims will replace all prior versions, and listings, of claims in this application.

1-18. (canceled).

19. (currently amended) A method of using a computer for ~~evaluating the ability of~~ selecting at least one of a plurality of chemical entities based on its ability to associate with ~~a molecule or molecular complex comprising~~ all or part of a calcineurin A (CnA) binding pocket defined by structure coordinates of CnA amino acids 90, 91, 92, 118, 120, 121, 122, 150, 151, 156, 160, 199, 232, 253, 254, 256, 281, 282, 283, 284, 306, 311, 312, and 317 according to Figure 1, or ~~a homologue of said molecule or molecular complex wherein said homologue comprises~~ a CnA homologue binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å;
wherein said computer comprises a machine-readable data storage medium comprising a data storage material encoded with said structure coordinates defining all or part of said binding pocket and wherein said method comprises the steps of:

a) utilizing said structure coordinates defining all or part of said binding pocket and the structure coordinates of one of said plurality of chemical entities to position a chemical entity within all or part of the CnA binding pocket or the CnA homologue binding pocket;

b) ~~performing a fitting operation between~~ docking said chemical entity with all or part of ~~and~~ the CnA

binding pocket or the CnA homologue binding pocket by employing computational means which utilize said structure coordinates of all or part of the binding pocket or the chemical entity, wherein said docking utilizes energy minimization;

c) analyzing the results of said ~~fitting operation~~ docking to quantify the association between said chemical entity and all or part of the CnA binding pocket or the CnA homologue binding pocket;

d) optionally repeating steps a) through c) with another of said plurality of chemical entities; and

e) selecting at least one of said plurality of chemical entities that associates with all or part of the CnA binding pocket or the CnA homologue binding pocket based on said quantified association of said chemical entity.

20. (currently amended) A method of using a computer for ~~evaluating the ability of~~ selecting at least one of a plurality of chemical entities based on its ability to associate with all or part of ~~a molecule or molecular complex comprising~~ a CnA binding pocket defined by structure coordinates of CnA amino acids 90, 91, 92, 118, 120, 121, 122, 150, 151, 156, 160, 199, 281, 282, 283, 306, 311, 232, and 254 [[,]] according to Figure 1, or ~~a homologue of said molecule or molecular complex, wherein said homologue comprises~~ a CnA homologue binding pocket that has a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5Å;

wherein said computer comprises a machine-readable data storage medium comprising a data storage material encoded with said

structure coordinates defining all or part of said binding pocket and wherein said method comprises the steps of:

a) utilizing said structure coordinates defining all or part of said binding pocket and the structure coordinates of one of said plurality of chemical entities to position a chemical entity within all or part of the CnA binding pocket or the CnA homologue binding pocket;

b) ~~performing a fitting operation between~~ docking said chemical entity with all or part of ~~and~~ the CnA binding pocket or the CnA homologue binding pocket by employing computational means which utilize said structure coordinates of all or part of the binding pocket or the chemical entity, wherein said docking utilizes energy minimization;

c) analyzing the results of said docking ~~fitting operation~~ to quantify the association between said chemical entity and all or part of the CnA binding pocket or the CnA homologue binding pocket;

d) optionally repeating steps a) through c) with another of said plurality of chemical entities; and

e) selecting at least one of said plurality of chemical entities that associates with all or part of the CnA binding pocket or the CnA homologue binding pocket based on said quantified association of said chemical entity.

21. (currently amended) A method of using a computer for ~~evaluating the ability of~~ selecting at least one of a plurality of chemical entities based on its ability to associate with all or part of ~~a molecule or molecular complex comprising~~ a CnA/CnB binding pocket defined by structure

coordinates of CnA amino acids 122, 124, 159, 160, 310, 312, 313, 314, 339, 341, 343, 344, 345, 347, 351, 352, 353, 354, 355, 356, 359, 360, and 363; and calcineurin B (CnB) amino acids 49, 50, 114, 115, 118, 119, 121, 122, 123, 124, 157, 158, 159, 161, and 162 according to Figure 1, or ~~a homologue of said molecule or molecular complex, wherein said homologue comprises~~ a CnA/CnB homologue binding pocket that has a root mean square deviation from the backbone atoms of said CnA and CnB amino acids of not more than 1.5Å;

wherein said computer comprises a machine-readable data storage medium comprising a data storage material encoded with said structure coordinates defining all or part of said binding pocket and wherein said method comprises the steps of:

a) utilizing said structure coordinates defining all or part of said binding pocket and the structure coordinates of one of said plurality of chemical entities to position a chemical entity within all or part of the CnA/CnB binding pocket or the CnA/CnB homologue binding pocket;

b) ~~performing a fitting operation between~~ docking said chemical entity and the CnA/CnB binding pocket or the CnA/CnB homologue binding pocket by employing computational means which utilize said structure coordinates of all or part of the binding pocket or the chemical entity wherein said docking utilizes energy minimization;

c) analyzing the results of said docking ~~fitting operation~~ to quantify the association between said chemical entity and all or part of the CnA/CnB binding pocket or the CnA/CnB homologue binding pocket;

d) optionally repeating steps a) through c) with another of said plurality of chemical entities; and

e) selecting at least one of said plurality of chemical entities that associates with all or part of the CnA/CnB binding pocket or the CnA/CnB homologue binding pocket based on said quantified association of said chemical entity.

22. (currently amended) ~~The~~ A method ~~according to claim 19 or 20,~~ of using a computer for selecting at least one of a plurality of chemical entities based on its ability to associate with all or a part of ~~wherein said molecule or molecular complex further comprises~~ a ~~second~~ binding pocket defined by CnA amino acids 90, 91, 92, 118, 120, 121, 122, 124, 150, 151, 156, 159, 160, 199, 232, 253, 254, 256, 281, 282, 283, 284, 306, 310, 311, 312, 313, 314, 317, 339, 341, 343, 344, 345, 347, 351, 352, 353, 354, 355, 356, 359, 360, and 363; and CnB amino acids 49, 50, 114, 115, 118, 119, 121, 122, 123, 124, 157, 158, 159, 161, and 162[[;]] according to Figure 1, or ~~a homologue of said molecule or molecular complex, wherein said homologue comprises~~ a ~~second~~ homologue binding pocket that has a root mean square deviation from the backbone atoms of said CnA and CnB amino acids of not more than 1.5Å;
wherein said computer comprises a machine-readable data storage medium comprising a data storage material encoded with said structure coordinates defining all or part of said binding pocket and wherein said method comprises the steps of:

a) utilizing said structure coordinates defining all or part of said binding pocket and the structure coordinates of one of said plurality of chemical entities to

position a chemical entity within all or part of the CnA/CnB binding pocket or the CnA/CnB homologue binding pocket;

b) docking said chemical entity with all or part of the CnA/CnB binding pocket or the CnA/CnB homologue binding pocket by employing computational means which utilize said structure coordinates of all or part of the binding pocket or the chemical entity, wherein said docking utilizes energy minimization;

c) analyzing the results of said docking to quantify the association between said chemical entity and all or part of the CnA/CnB binding pocket or the CnA/CnB homologue binding pocket;

d) optionally repeating steps a) through c) with another of said plurality of chemical entities; and

e) selecting at least one of said plurality of chemical entities that associate with all or part of the CnA/CnB binding pocket or CnA/CnB homologue binding pocket based on said quantified association of said chemical entity.

23. (currently amended) A ~~The~~ method ~~according to claim 22,~~ for using a computer for selecting at least one of a plurality of chemical entities based on its ability to associate with all or part of a ~~wherein said~~ molecule or molecular complex ~~is~~ defined by the entire set of structure coordinates of CnA/CnB amino acids according to Figure 1, or a homologue thereof, wherein said homologue has a root mean square deviation from the backbone atoms of said CnA and CnB amino acids of not more than 1.5Å;

wherein said computer comprises a machine-readable data storage medium comprising a data storage material encoded with said structure coordinates defining all or part of said molecule, molecular complex, or homologue thereof and wherein said method comprises the steps of:

a) utilizing said structure coordinates defining all or part of said molecule, molecular complex, or homologue thereof and the structure coordinates of one of said plurality of chemical entities to position a chemical entity within all or part of the molecule, molecular complex, or homologue thereof;

b) docking said chemical entity with all or part of the molecule, molecular complex, or homologue thereof by employing computational means which utilize said structure coordinates of all or part of the molecule, molecular complex, or homologue thereof or the chemical entity, wherein said docking utilizes energy minimization;

c) analyzing the results of said docking to quantify the association between said chemical entity and all or part of the molecule, molecular complex, or homologue thereof;

d) optionally repeating steps a) through c) with another of said plurality of chemical entities; and

e) selecting at least one of said plurality of chemical entities that associate with all or part of the molecule, molecular complex, or homologue thereof based on said quantified association of said chemical entity.

24. (currently amended) The method according to claim 23 ~~22~~, wherein said ~~molecule or~~ molecular complex ~~comprises~~ is defined by the structure coordinates of the amino acids ~~17-392~~ of CnA, the amino acids ~~1-169~~ of CnB, ~~intact~~ FKBP12 and FK506 according to Figure 1, or a homologue thereof, wherein said homologue has a root mean square deviation from the backbone atoms of said CnA and CnB amino acids of not more than 1.5 Å.

25. (previously presented) A method for identifying a compound capable of associating with a molecule comprising a CnA-like binding pocket comprising the steps of:

a. using the atomic coordinates of CnA amino acids 90, 91, 92, 118, 120, 121, 122, 150, 151, 156, 160, 199, 232, 253, 254, 256, 281, 282, 283, 284, 306, 311, 312, and 317 according to Figure 1 ± a root means square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, to generate a three-dimensional structure of a molecule comprising a CnA-like binding pocket;

b. employing said three-dimensional structure to design or select said compound;

c. synthesizing said compound; and

d. contacting said compound with said molecule to determine the ability of said compound to interact with said molecule.

26. (previously presented) A method for identifying a compound capable of associating with a molecule comprising a CnA-like binding pocket comprising the steps of:

a. using the atomic coordinates of CnA amino acids 90, 91, 92, 118, 120, 121, 122, 150, 151, 156, 160, 199, 281, 282, 283, 306, 311, 232, and 254 according to Figure 1 ± a root means square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, to generate a three-dimensional structure of a molecule comprising a CnA-like binding pocket;

b. employing said three-dimensional structure to design or select said compound;

c. synthesizing said compound; and

d. contacting said compound with said molecule to determine the ability of said compound to interact with said molecule.

27. (previously presented) A method for identifying a compound capable of associating with a molecule comprising a CnA/CnB-like binding pocket comprising the steps of:

a. using the atomic coordinates of CnA amino acids 122, 124, 159, 160, 310, 312, 313, 314, 339, 341, 343, 344, 345, 347, 351, 352, 353, 354, 355, 356, 359, 360, and 363; and CnB amino acids 49, 50, 114, 115, 118, 119, 121, 122, 123, 124, 157, 158, 159, 161, and 162 according to Figure 1 ± a root means square deviation from the backbone atoms of said amino acids of not more than 1.5 Å, to generate a three-dimensional

structure of a molecule comprising a CnA/CnB-like binding pocket;

b. employing said three-dimensional structure to design or select said compound;

c. synthesizing said compound; and

d. contacting said compound with said molecule to determine the ability of said compound to interact with said molecule.

28. (previously presented) The method according to claim 25 or 26, wherein in step a), the atomic coordinates of a second binding pocket defined by CnA amino acids 122, 124, 159, 160, 310, 312, 313, 314, 339, 341, 343, 344, 345, 347, 351, 352, 353, 354, 355, 356, 359, 360, and 363; and CnB amino acids 49, 50, 114, 115, 118, 119, 121, 122, 123, 124, 157, 158, 159, 161, and 162 according to Figure 1 ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å are used.

29. (previously presented) The method according to claim 28, wherein in step a), the atomic coordinates of the entire set of structure coordinates of CnA and CnB according to Figure 1 ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å are used.

30. (currently amended) The method according to claim 28, wherein in step a), the atomic coordinates of the amino acids ~~17-392~~ of CnA, the amino acids ~~1-169~~ of CnB, ~~intact~~

FKBP12 and FK506 according to Figure 1 ± a root mean square deviation from the backbone atoms of said amino acids of not more than 1.5 Å are used.

31. (currently amended) The method according to any one of claims 19, 20, ~~and~~ 21 and 22 prior to step a), further comprising the steps of:

a) producing a crystal of a molecule or molecular complex comprising amino acids 5-168 of CnA and amino acids 24-370 of CnB ~~CnA/CnB~~ and a chemical entity;

b) determining the three-dimensional structure coordinates of the molecule or molecular complex by X-ray diffraction of the crystal; and

c) identifying all or part of said binding pocket.

32. (currently amended) The method according to any one of claims 25, 26 and 27 prior to step a), further comprising the steps of:

a) producing a crystal of a molecule or molecular complex comprising amino acids 5-168 of CnA and amino acids 24-370 of CnB ~~CnA/CnB~~ and a chemical entity;

b) determining the three-dimensional structure coordinates of the molecule or molecular complex by X-ray diffraction of the crystal; and

c) identifying all or part of said binding pocket.

33. (currently amended) The method according to any one of claims 19, 20 and 21 wherein the docking ~~fitting operation~~ utilizes ~~energy minimization,~~ shape complementarity or is followed by molecular dynamics.

34. (currently amended) The method according to any one of claims 19, 20 and 21 wherein the docking ~~fitting operation~~ is performed through visual inspection on a computer screen using a computer program capable of generating a three-dimensional graphical representation of said structure coordinates and structure coordinates of said chemical entity.